

FIGURE 1

CGGACGCGTGGGACCCATACTGCTGGTCTGATCCATGCACAAGGCAGGGCTGCTAGGCCTC
TGTGCCCGGGCTTGAATTGGTGCAGGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATGGCTCGCCATGCCCGGC
GTTTGGCCCAGGACGGGGCCCATGTGGTCGTCAGCAGCCGAAGCAGCAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGAGGGCTGAGCGTGACGGCACCGTGTGCCATGTGGGGAA
GGCGGAGGACCGGGAGCGGCTGGTGGCACGGCTGTGAAGCTTATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTCAACCCCTTCTTGGAAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAACGAGGAGGCGGCTCAGTGGTATCGTGTCTTCATAGCAGCCTCAGTC
CATCTCCTGGCTTCAGTCCTACAATGTCAGTAAAACAGCCTGCTGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAACACTGCCTAGCACCTGGACTTATCAA
GACTAGCTTCAGCAGGATGCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC
TGC GGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTCCTGTGCTCT
GAAGATGCCAGCTACATCACTGGGAAACAGTGGTGGTGGAGGAACCCGTCCCGCCT
CTGAGGACCGGGAGACAGCCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGTGTTCTGC
ATTCA CCCACTGGCCTTCCCACCTCTGCTCACCTTACTGTTCACCTCATCAAATCAGTTCT
GCCCTGTAAAAGATCCAGCCTCCCTGCCGTCAAGGTGGCGTCTACTGGGATTCTGCT
GTTGTTGTGGCCTTGGTAAAGGCCTCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT
GAGTCTACCTGGCAAAGACCAAGATATTTTCTGGCCACTGGTGAATCTGAGGGGTGA
TGGGAGAGAAGGAACCTGGAGTGGAGGAGCAGAGTTGCAAATTAAACAGCTGCAAATGAGG
TGCAAATAAAATGCAGATGATTGCGCGGCTTGAAAAA

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVVS
SRKQQNVDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLDINVKAPALMTKAVVPEMEKRGGGSVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC
AGIVSFLCSEDASYITGETVVVGGGTPSRL

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

FIGURE 3

GCGCCCTGAGCTCCGCCTCCGGGCCCGATAGCGGCATCGAGAGCGCCTCCGTGAGGACCAGGCAGCG
 CAGGGGGCCGGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCCTGCAGAACCAAGTGGC
 GCGGCTGGAGGAGGAACCGAGACTTCTGGCTGCCCTGGAGGACGCCATGGAGCAGTACAAACTGC
 AGAGCGACCAGGCTCGTGAGCAGCAGGAGGAGATGGTGAACTGCGGCTGCCTTAGAGCTGGTGC
 CCAGGCTGGGGGGCCTGCCCTGAATGCCCTGCCCTCCGGCTTGTGCCTCGACCTCATAC
 AGCCCCCTGGGGGTGCCACGCCATGTGCTGGCATGGTGCCTGCCCTGCCCTCCCTGGAGATG
 AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT
 GAGGTGAACAGGCTGGGAAGTGGCTTCAGCTGCTCAGAGGAGGAAGAGGAGGAGGAGGCC
 CAGGCGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGGGGGCACGCCAG
 GGAGTCTGCCAGAGAGGAAGGCCAGAGCTTGCTGAGGAGTTGGATGCAGCCATTCCAGGGTCC
 AGAGCAGTTGGTGGGAGCAAGGCCAGGCTCAGGCCAGGCCCCCTGCCACAGCCTCAGAGTG
 GCGGCTGGCCCAGGCCAGCAGAAGATCCGGAGCTGGCTATCAACATCCGATGAAGGAGGAGCTTA
 TTGGCGAGCTGGTCCGCACAGGAAAGGAGCTCAGGCCCTGAACGCCAGCACAGCAGCGTATCCGG
 GAGCTGGAGCAGGAGGAGCAGGAGCAGGTGCGGGCGAGCTGAGTGAAGGCCAGGGAGCTGCC
 CGAGGGCAAGGAGCTCAGGATGCTGGCGAGCGGTCTGGCTCCAGGAGTTCCGCAGGAGGGTGC
 CGGCCAGAGCCAGGTGCTGAAGGAGAAGAACAGCAGGCTACGGAGCGGCTGGTGTCACTGTC
 GCCCAGAGTGAAGCAGTCAGAGCTCGAGCGAACGTGCAGCTCATGCCAGCAGCAGGGACA
 GCTGCAGAGGCCGCTCGCGAGGAGACGGAGCAGAAGGCCGCTGGAGGAGAAATGAGCAAGCG
 AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATAAGAC
 GAGATCGCGGCCCTCCAGAGGAAGAGGCGCAGTGGCAGCAACGCTCTGGTGTCAAGCTGG
 GCAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAG
 CGCTGGAGGAGCTGGGAGGAGCTCCACAAGCGGAGGCCATCTGGCAAGAAGGAGGCC
 CAGGAGAAGACGGGCTGGAGAGCAAGGCCCTGAGATCCAGGCCAGGCCCTCAACGAG
 AGTGTCCAGGCCGCTGGAGCACCTGGAGAAGGAGCTGTCAGAGAGAGCAGCTGCC
 GCGCCAGAGCCAGCAGCAGATCCGCGGGAGATCGACAGCCTGCCAGGAGAAGGACTCG
 AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGAGTCTGCTGTCCCCGAGGAG
 GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGA
 ATGAGGCCATCA
 CATGCCAGGGTCTGGGCCCTAGGCCCTGTTGCTGTCCCAGTGCAGAGATGAACCTCATGCC
 AAGCTCAGCTACCTCTCATCCTCAGAGACCAGAGGCCCTCTGCAAGTATTTGACAAG
 GTGGTACAGCAGCAGCAGGAGGAGCTGAGGAGGAGTATGAGGCCATTCAAGCT
 CTGGAGAAGGAACACTGGGAGGAGCAGCTGGAGGAGGAGCAGCTGGAGGAG
 ACATGTGGATAAACCAAGGAACAGAACAGAACAGCTGGAGGAGGAG
 GGGGAGAAGAGGAGCCTGTGCTCGAGGGCAGACAGGCTCTGGAAATGAAG
 ATGAGCTCCACCTGGC
 ACCCGAGCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCAGGGAGACGCC
 TGGTCACGCTCCGTTACCCCTGACCTGGAAACGCTCGAGCCTGTGAGGAG
 GAGGAAGGAGCAGGCCCTGGAGGAGGAGCTGAGGCCAGGAG
 CCTGCCCTGGAACTTTGGCCTTGTCCAAGGCCCGGGAACTGCGACGCC
 TTGATGTCCGGAAAACCCCTGTAAGCCCTGCCAGACCCCTGCC
 GCTGAAAGGGCAGCTGCCCTGGTGAAGGGAGTCCCTACCG
 CCCTCATCTGTACCCCTCACTGGGATCAACAAATTGGCC
 AACAAATAATATGCAAATTCCCACCACTTACTTCC
 TCTGCTGAAGGGAGTCCCTGGAGGAGACTCCAG
 GCAAGAATCATCACGAAAGGGTGGCAACCAGGGTGTGG
 GAAACTGGAGACTTTAGGATCTTAAAAACCA
 TAATAAAAAAAATCTTGAAGGGAC

FIGURE 4

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465
<subunit 1 of 1, 830 aa, 1 stop
<MW: 95029, pI: 8.26, NX(S/T): 2
MEQYKLQSDRLREQQEEMVELRLRLELVRPGWGLRLLNGLPPGSFVPRPHTAPLGGAHAV
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL
HLRRNRISNCQRAGARPGSLPERKGPELCLEELDAATPGSRAVGGSKARVQARQVPPATAS
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQVLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQQGQLQRRLREETEQKRRLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQRKRRSGSNGSVSLEQQQKIEEQQKWLDEQEMEKVLQQRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAQSQQQIRGEIDS
LRQEKDSSLKQRLEIDGKLQRGSLLSPEEERTLFQLDEAIEALDAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMALKSYLSSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLEEQQR
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLQQSRDHLCGEGLADSRRQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVHSRGGEKRSLCSEGRQAPGNEDELHLAPELLWLSPLTEG
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL
```

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCTCCTAGAGCATTTGGAAGCATGAGGCCACGATGCTGCATCTGGCTCTGTCTGCT
GGATAACAGTCTCCTCCAGTGTCAAAGGAACACTACAGACGCTCCTGGCTCAGGA
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGAAACAAGATCTACAACCCTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTAAAGGAGACCCGCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTGAGCTCTGCTGTCCCAGTCTTGGCCCCAGCAGAAGTTCTGTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCATCTCCGGAGCTGTAC
CAGGAACAGGAGGCACGTCTGTACCCAAAAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACCTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTGGAGAGGAGCCAGCTGGGATGGC
CAGACTTCAGGGGAAGAATGCCTCCTGCTTCATCCCCTTCCAGCTCCCCTCCGCTGAG
AGCCACTTCATCGGCAAAAAACCCACATTACCATCT

20033346 322701

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700
><subunit 1 of 1, 125 aa, 1 stop
><MW: 14198, pI: 9.01, NX(S/T): 1
MRPRCCILALVCWITVFLLQCSKGTTDAPVGSGLWLQOPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRLGMKSQCHLSPISRSCTRNRRHVLYP
```

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

FIGURE 7

CCCACGCGTCCGCCACGCGTCCGGTGCACACTCGCGCGCCGCGCTCCGGCTCTCT
 TTTCCCTCCGACGCGCACGGCTGCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG
 AACCCCTCCGCGGAGAGGAGCGAGGCGGCCAGGGTGGCCCCGGGGCGCGCTGGTCTCG
 GAGAAGCGGGGACGAGGCCGGAGGGATGACCGACTGAGGGCGACGCCGGCACTGACGCCAGTT
 GGGGCCGCGACTACCAGCAGCTGACAGCGCGATGACCGACTCCCCAGAGACGCCCTAGCCCG
 GTGTGCGCGCCAGGCCGGAGCGCGCAGGTGGGCTGGCTGTTAGGGTCCGCCAACGCCGG
 TCGCCGGCCGCCAGGATGGCGCTGGCAACCCGGCCGCGCCGCTGCTACCCCTG
 CGCCCGCTGCGAGCCGGCGTCCGGCCCGCCGCTGCGCTCATGGACGGCGCTCCCGCTG
 GCGCGGCCGCCGGCTGTGAATGCGACTGCCCTCGGCCGCGCTCCCCGCCGCC
 GCCCGCCGGACGTGGTAGGGG**ATG**CCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
 GTTCCCTCCTGGTCACCTGCTGCCGTGGCTCTGCAAGTCCGAGCAGCTGGAG
 AAGCTGGCCCAGGCACCAGAGCAGCCGGCCAGGAGAAGCGTGAGCACGCCACTGGACGG
 CCCGGGGCGGGTAACGAGCTCGGCGCCCGCGAGGGACGAGGGCGGAGCGGCCGGACT
 GGAAGAGCAAGAGCGGCCGTGGCTGCCCGCGTGAAGCTGAAGCAGGAC
 TGGGTCTCCAGGGCGGGGCCAAGGCCGGGATCTGCAGGTCCGCCCGCGGGACAC
 CCCGCAGGCGGAAGCCCTGGCCGAGCCGCCAGGACGCGATTGGCCCGGAACCGCC
 CGCCCGAGCCACCCGAGGAGTACGTGTACCGGACTACCGTGGCAAGGGCTGCGTGGACGAG
 AGCGGCTTCGTGTACCGATCGGGAGAAAGTTCGCCGCCGGCCCTGGCCTGCCGTGCCT
 GTGCACCGAGGAGGGGCCGTGTGCGCGCAGCCGAGTCCGAGGCTGCACCCGCGCTGCA
 TCCACGTCGACACGCCAGTGCCTGCCCGAGTGAAGGAGAGGAAGAACTACTGCGAGTT
 CGGGCAAGACCTATCAGACTTGGAGGAGTTCTGTGGTCTCCATGCGAGAGGTGTGCTG
 TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTG
 CTGTGTACGAGCCTGATCAGTGCCTGCCATCTGCAAAATGGTCAAACACTGCTTGAGAA
 ACCCGGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGACCCATGCCACTGTAC
 TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC
 AAATG**TAG**ACGCTTCCAGAACACAAACTCTGACTTTCTAGAACATTTACTGATGTGAA
 CATTCTAGATGACTCTGGAACTATCAGTCAAAGAAGACTTTGATGAGGAATAATGGAAA
 TTGTTGGTACTTTCTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTC
 AAAACATCAACAAGAACACTTGGCATAAAATCCTCTCTAAATAATGTGCTATTTCACAG
 TAAGTACACAAAAGTACACTATTATATCAAATGTATTCTATAATCCCTCCATTAGAGAG
 CTTATATAAGTGTGTTCTATAGATGCAGATTAAGGAAATGCTGTGTTGCAACCGTAAAAAA
 AAAAAAAAAAAAAAA

FIGURE 8

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818
><subunit 1 of 1, 325 aa, 1 stop
><MW: 35296, pI: 5.37, NX(S/T): 0
MPSSTAMAVGALSSSLVTCLMVALCSPSIPLEKLAQAPEQPGQEKRHATRDGPGRVNEL
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AAAQDAIGPELAPTPEPPEYVYPDYRGKGCVDSEGFVYAIIGEKFAPGPSACPCLCTEEGPL
CAQPECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEEGTWR
IERQAMCTRHECRQM
```

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGTTATTACTGCTGCCCTCCTGGGTTCATCCTCCCAC
TGCCAGGAGTGCAGGCCTGCTCTGCCAGTTGGACAGTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCAACTGAGCCTGGTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGCCTCCCTGATC
TCCTACACCTTCTGCTGCCGCCAGGAGGGACTCTGCAACAAACCTCGTTAACCTCCCTCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGACAACAGAAAGAGATCTGCCCAAGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
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ACTGCAATAGGAAAGATTCTGACCTGTCATCGGGGACCACCATTATGACACACCGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCAGGT
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCCTGGTGGGACAAAAG
GCTGCAGCACTGTTGGGCTCAAATTCCCAGAAGACCACCATCCACTCAGCCCTCCTGGG
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACCTCCCTCCCTCAAGCTGCCCTGTCCCAGGAGACCGCAGTGTG
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GGCGCCACTCATTGTTATGATGGGTACATTCTCTCAGGAGGTGGCTGTCCACCAAAAT
GAGCATTCAAGGCTGCGTGGCCAACCTCCAGCTTCTGTAAGCTGAGGAGACACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCGAGCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACCTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTG
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CCATTCTGTCCATGAATCATCTCCCCACACACAATCATTCAATCTACTCACCTAACAGCA
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GCTGCATGTATCTGATAATACAGACCCTGTCCCTTCA

FIGURE 10

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ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTCYDGLLRLRGGGIFSNLRVQGCMPPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGPKGCVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSVLLN
SLPPQAAPVPVGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACGATGCTACGCGGCCGGCTGCCTCCGACCTCCGTAGCGCCTGCCGCCCTG
GCTCGGGCGCTGCTCTCGCTGCGCTGCTCTCTTAGAGCCGAGGGACCCGGTGGC
CTCGTCGCTCAGCCCCATTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCGTGCTAT
TGTCGGGCCCGAGGCTCCGTGGCGGGACCCTGAGCTGCTGGAGGGACCTGCACCCGGTGG
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GCAGCCCGCACCTGGGTGCGCGCTGGCGACTGGCTTGTGGTACGCGGACTGGATGGAC
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCACAGCTGGCGCTGCCTGGCCTCGCT
CTTCCCGGCCCTTTCAGCCGTGAGAACTACGCCGCCTGCAGGGCTGTGGCAGCACTACCACCCCTGGC
ACCGCTGCATGGATAGCAGCGCCCTTCCCTGCAGGGCTGTGGCAGCACTACCACCCCTGGC
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ACTTTGCAAGTGCAGTAAATGATTAAATGCAGATTAACTCAAGTAGCCTTTCACCTG
TTCATTGACCTGGCAATTAAAGGTGTTAAATCTCCTGGTGTGATGTTTGACATAGATG
ATGCAAAGGTATTAGAATATTAAATGATCTGAAACAATATTGAAAAGAGGATATGGGTAT
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FIGURE 12

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RDLGAALADWPLWYADWMGDQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL
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Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

2003232345 2003232345
FIGURE 13

GGGACTACAAGCCGCCCGCTGCCGTGGCCCTCAGCAACCTCGACATGGCGCTGAGGCAGGCCACCGCGAC
TCCGGCTCTCGCCTCGGCTGCCGTACTCTTCCTGCTGCTGCTTTCAAGGGCTGCCGTATAAGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGAAACTGTCTGCATCATTACGGATTCGC
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATCAAGATGAACAAACCACATAIGTGTGTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTGTGAGAAATACTGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTGTGAAATGACCGCAAGGAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCAGGCTGTACAGTGGTATCGCAATGATGTACCACTGCCACGGATT
ACTGCCAGGAGAGTGAGGGCAGCCCCGGCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCAGATTGCAATTCTCTTCACTTAAACTCTGAAACAGGCACCTTGGTGTTCACTGCTG
TTCACAAGGACACTGGGCACTACTGCAATTGCTTCAATGACCGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAAACATTGGCGGAATTATTGGGGGTTCTGGTGTCTGCTGACTGGCCCTGA
TCACGTTGGCATTGCTGTGCATACAGACGTGGTACTTCATCAACAATAAACAGGATGGGAAAGTTACAAGA
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCAGTTCAAGACACAAGTCATGTTG
TGATCTGAGACCCCGGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAGAAAGCTTTCTGTTGGCCAAAGTGTACCA
CTACTCTCTTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCACAA
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GTAAATTGGTGTGAAAGAGGGATCTGGCTGAGGAACCTGCTTGTCCAACAGGGTGTCAAGGATTTAAGGAA
ACCTTGTCTTAGGCTAACTGTAAGTGTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGTGTTATTTATAAAATT
TACATCTAAATTGGTAAAGGATGTATTGATTATTGAAAAGAAATTCTATTTAAACTGTAATATATTGT
CATACAATGTTAAATAACCTATTTTAAAGGTTCAACTTAAGGTAGAAGTCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAAAGATTTACCAAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTTCT
CACACAAGTTTACGCTTTTCAAGGGAACTCATACTGTCACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCATCTCTCAAAAGAAACCTCTCAGGTTAGCTTGAAC
GCCTCTCCTGAGATGACTAGGACAGCTGTACCCAGAGGCCACCCAGAACGCCCTCAGATGTACATACAGATG
CCAGTCAGCTCCTGGGTTGCGCCAGGCAGCCCTCTAGCTCACTGTTGCCCTGCTGTGCCAGGAGGCCCT
GCCATCCTGGGCCCTGGCAGTGGCTGTCCCAGTGAGCTTACTCAGTGGCCCTTGCTTCACTCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTGGCTCCTGTAACAGACCTCT
TTTGGTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTTTTAAGTTGTTAATTATTGTT
AAGATTGTCTAAGGCCAAGGCAATTGCAAATCAAGTGTCAAGTACAATAACATTAAAGAAAATGGAT
CCCACTGTTCTCTTGCACAGAGAAAGCACCAGACGCCACAGGCTCTGCGATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGGCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG
TGAAACGCCATGAACTCAAAGCAGTTCTAATTGACTTTAAATTGTTATGAAACACTTGGCCAGGCCCTGGCAGAGGCA
GGAAATGCTCCACCGAGTGGCTCAGTGCCTCCCTGGTGTCTGCGCATGGCATCTGGATGCTTAGCATGCAAGTTC
CCTCCATATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTGGGGATTCAACGCTCCAGCCTCCT
TCTTGGTTGTCAGTGATAGGGTAGCCTTATTGCCCTCTTAAACCTTACACTAGTGC
TGGGAAACCAGGTGTGAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGGTGTGTCACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTTATAAAAGCTCAAAAAACCA

FIGURE 14

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCI ITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 15

CAGGACCAAGGTCTCCTACGCTGGAGCAGCGGGAGACAGCCACCATGCACATCCTCGTGGTCATGCCATGGTG
ATCCTGCTGACGCTGGCCCCCTCGAGCCGACGACAGCGAGTTCCAGGCCTGCTGGACATCTGGTTCCGGAG
GAGAAGCCACTGCCACCGCCTCCTGGACACATCGGAGGAGGCCTGCTGGCTTCCCTGACTGGCTGAAGCTG
CGCATGATCCGTTCTGAGGTGCTCCGCTGGACGCCCTGCAGGACCTGGAGGCCGACAGCTGCTGCTG
TTCGTGAGTCGTTGGCATCCCGTGTCCAGCATGAGCAAACCTCTCCAGTTCTGGACCAGGCAGTGGCCCAC
GACCCCAAGACTCTGGAGCAGAACATCATGGACAAGAAATTACATGGCCACCTGGTGGAGGTCCAGCATGAGCG
GGCGCCTCCGGAGGCCAGACTTCCACTCCTGCTCACAGCCTCCCTGCCGCCCGAGACAGCACAGAGGC
CCCAAACCAAGAGCAGCCAGAGCAGCCATAGGCAGGGCCGGATTGGGTGGGACCCAGCTCCGGTGCTG
GCCCTGAGGACGACCTGGCTGGCATGTTCTCCAGATTTCCGCTCAGCCGGACCTCGGTGGCAGAGCTG
AGTCCCCGCCCGTGGCCCTGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCGTGTCCAGGGAGCC
GAGGTGCCGGCATCAGGTGCGTGTCCCTGCCACCCCTGCTCAGCTCCCCACACGGCGGTGCCCTG
GTGATGTCCATGCACCGTAGCCACTTCTGGCTGCCGCTGCGCAGCTGCCAGTACCGCGTGTGTG
CCACAGGACACCGGCTTCTCGCTCTCGTAAGGTGCTCCAGATGCTGAGTGGCTGGACAGCCCTGG
GTGGAGGGGGCCCTGCGGGCACAGCTCAGGATGCTTGCAGGCCAGGCTCAGCCGGCGCAGGCTAGTGT
GTGCGAGGGGGCTCCTGCGCTGGCCAGGCCCTGGCTCAGGACCTGGAGGTGGTCAGCTCCACCGT
CGTCCGTCATGCCACCTGAGGTCTGGGAGCAGTGCAGCGTGGAGCCGACCTGATCAGCAAAGTCTCCAG
GGGCTGATGAGGTGAGGTCCCCCACCTGGAGGAGCTGACTGCAATTCTCTGCCACTGCGGATGCTGCC
TCCCCGTTCCAGCCTGTAAGCCCCTGGTGGTGGAGCTCCCTGCTGCTGCAGGAGGAGGCCCTGGCTGGG
GGGAAGCCGGGTGCGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGCCCTGTCAGGCCCTCCTAGTGGACTGG
CTGGAAATGCTGGACCCCGAGGTGGTCAGCAGCTGCCCGACCTGCAAGCTCAGGCTGCTCTCCGGAGGAAG
GGCAAAGGTCAAGGCCAGGTGCCCTGTTCCGCTCCACCTCCAGGCTGCTGCTCAGCTCAGTCCAGTGGGCC
ACACTGCACCAAGTCATCCAGTCCTGCTGGCAAGAGGCCGAACAGAGGTTGACCCCTCTGCCCTCTGGAC
TTCCCTGGGCTGCACTCATGTTCTCGCATCTGGCAGGGCCGGGACCGCGCACCCCGAGACGGCGGGAG
GAGCTGGTCTGCCGGTCCAGGGCCGGAGCTCATCAGCCTGGAGCTGATCTGGCCAGGCGAGACGCCGG
AGCCAGGACGGGACACAGCCGCTGCAGCCTCATCCAGGCCGGCTGCCCTGCTGCTCAGCTGCTGTGGG
GACGATGAGAGTGCAGGAAGGTGACGGAGCACCTGTCAGGCTGCATCCAGCAGTGGGAGACAGCGTGTGGG
AGGCCTGCCAGACCTCTCTGCAAGCTCACAGCGGCCGGAGCTGCCGGTGCCTGAGGTCTTA
CTGCACAGCAAGGGCTGCCAGCAGCAGCGTCTGCAAGCTGGACGGACTCATCCACCGCTCATCAGCTCCTT
GCCGACACCAGCACTCCGGCGTTGGAGAACCGAGGGCGGATGCCAGCATGCCCTGCCGAAGCTGGCGGTG
GCGCACCCGCTGCTGCTGCCACCTGCCATGATCGCGCGCTCTGCACGCCGACCCACCTCAACTTC
CAGGAGTTCCGGCAGCAGAACACCTGAGCTGCTTCTGCACTGCTGGGCTGTCAGGAGCTGCTGCAGCCGCAC
GTGTTCCGAGCGAGCACAGGGGGCGTGTGGACTGCCTCTGTCATCCGCTGCTGCTGAATTACAGG
AAGTCCCTCCGCCATCTGGCTGCCATCAACAAGTTGTGCAGTTCATCCATAAGTACATTACATACATGCC
CCAGCAGCCATCTCTCTGCAAGACGCCGACCCGCTCCACGACCTGCTTCAGCAACAGTGACCTGGTG
ATGCTGAAATCCCTCTGCAAGGGCTCAGCTGCCAGCAGGGACGACAGGACCGAGGCCCTGGACGAAGAG
GGCGAGGAGGAGAGCTCAGCCGGCTCCCTGCCCTGGTCACTGCTCCCTGTTCACCCCTCTGACCGGGCCGAG
ATGGCCCCCTACATGAAACGGCTTCCGGGCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGA
GAGATGCTCCGGGGAGACCCGAGATCTGAGCTTCTGACCAACCTGCAAGGGCTGATGAGCTGGCCGAG
GAGTGTGCGCAACCTCGCCTTCAGCCTGGGCTGCGCTCCATGCAAGACAGCCCCAGCATTGCA
CTGCCACGTTCATGACTGCCCTGGCAGGAGCTTGAGGTGGTCAGACGCCCTCCGAACCTGCTGAG
TACGCTCTCTGTCGCCAAGAGCACGCCGCTGCTGCCCTGCCACGGGCTTCTGTTGGCATGTA
GACCCAGCGCGAGATCTCGAGGGCCCTGAGGATCTGCACTGGAGGCCGTGATGAGCTGGCCAGCGA
CCCCCTCCAAGCCCCGGCCGCTCCGCTCCGGGATCTCGAGGCAAAGGCCAGGAAGCGTGGGCGTTGCTGG
TCTGTCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGAGCAATACTCCGAGGCCCTGGGGTGG
CTCCGGGCCGGCGCTGGCATCAGGGGCCGTCCAGCAAGCCCTCATCACCTCTGGGCCACAGGCCCTGCCGG
AGCGGGGGATCCCCCGGGCATGCCCTGGCTGGTTTGAATGAAACGACCTGAACCTGTCAA

FIGURE 16

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631
><subunit 1 of 1, 1029 aa, 1 stop
><MW: 114213, pI: 6.42, NX(S/T): 0
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MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPPKPKSSPEQPIGQGRIRVGTQLRVLG
PEDDLAGMFLQIFPLSPDPRWQSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLLSSPHGGALVMSMRSHFLACPLLRLQLCQYQRCVPQDTGFSSLFLKVLLQMLQWLDSRG
VEGGPLRAQLRMLASQASAGRRLSDVRGGLLRAEALAFRQDLEVSVSTRAVIATLRSGEQ
CSVEPDLISTKVLQGLIEVRSPHLEELLTAFFSATADAASPFPACKPVVVVSSLLLQEEEPLA
GGKPGADGGSLEAVRLGPSSGLLVDWLEMMDPEVVSSCPDLQLRLFSRRKGKGQAQVPSFR
PYLLTLFTHQSSWPTLHQCIRVLLGKSREQRFDPSASLDFLWACIHVPRIWQGRDQRTPQKR
REELVLRVQGPETISLVELILAEAEETRSQDGDTAACSLIQARLPLLLSCCCGDDESVRKVTE
HLSGCIQQWGDSVLGRRCRDLLLQQLYLRPELRVPVPEVLLHSEGAASSSVCKLDGLIHRFI
TLLADTSDSALENRGADASMACRKLAVAHPLLRLHLPmiaALLHGRTHLNQFQEFRQNHLS
SCFLHVGLLLELLQPHVFRSEHQGALWDCLLSFIRLLNYRKSSRHLAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDLSFDNSDLVMLKSLLAGLSPSRDDRTDRGLDEEGEEESSAG
SLPLVSVSLFTPPLTAAEMAPYMKRLSRGQTVEDLLEVLSIDEMSRRLPEILSFFSTNLQRL
MSSAEECCRNLAFSLALRSMQNSPSIAAFLPTFMYCLGSQDFEVVQTALRNLPEYALLCQE
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM
```

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 17

CCGGGCCATGCAGCCTGGCCCCGGCGGCCGCGCACCCGAGGAGA**TGAGGCTCCGC**
AATGGCACCTCCTGACGCTGCTCTCTGCCTGTGCGCCTCCTCGCTGTCCTGGTA
CGCGGCACTCAGCGGCCAGAAAGGCGACGTTGTGGACGTTTACCAAGCGGGAGTTCCCTGGCGC
TGCGCGATCGGTGACCGAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTAACCTG
GTGCTGGACGAGATCAAGAGGGCCGTGTCAAGAAAGGCAGGCCTGCGAGACGGAGACGGCAA
TCGCACCTGGGCCGCTAACAGAGGACCCCCGATTGAAGCCGTGGAACGGCTCACACCGGC
ACGTGCTGCACCTGCCAACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT
CTGCAGCCCAGGTGCGCGTGGGCCAGGGCGCACCGGAGTGTGCGTGGTGTGGCATGGGATCCC
GAGCGTGCAGGTGACTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGC
TGAGCCCGCAGGAGAAGGAGGACTCGGTATCGTGGTGTGATGCCGAGACTGACTCACAG
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTGTTCCCCACGGAGATCCATTCTGGGCT
CCTGGAGGTATCTCACCCCTCCCCCCTACCTCACCCCTGACTTCTCCGCCCTCCGAGAGTCCT
TTGGGACCCCAAGGAGAGAGTCAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCCTC
ATGATGTACGCGCAGTCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA
GCCCAACTACCTGAGCACCATGAAGAACATTGCACTGCAGCAGCCTCAGAGGACTGGATGA
TCCTGGAGTTCTCCAGCTGGCTTCATTGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG
ATTGTAGAGTTCATCTCATGTTCTACCGGACAAGCCCATCGACTGGCTCCTGGACCATA
TCTGTGGGTGAAAGTCTGCAACCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA
ACCTGCGGATCCGCTTCAAACCGTCCCTTCCAGCACGTGGGACTCACTCCTCGTGGCT
GGCAAGATCCAGAAACTGAAGGACAAAGACTTGGAAAGCAGGCCTGCGGAAGGAGCATGT
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATAACAGCACTCACCCCTGGAGAAAG
CCTACCTGCGCGAGGACTTCTCTGGCCTTCACCCCTGCCGCGGGGACTTCATCCGCTTC
CGCTTCTCCAACCTCTAACAGACTGGAGCGGTTCTTCTCGCAGTGGAACATCGAGCACCC
GGAGGACAAGCTCTAACACAGTCTGTGGAGGTGCTGCCCTCGACAACCCCTCAGTCAGACA
AGGAGGCCCTGCAGGAGGGCCGACCGCCACCCCTCCGGTACCCCTGGAGCCCCGACGGCTAC
CTCCAGATCGGCTCTTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTCGGCC
TCTGGAAGCACTGCGCTCTCGATCCAGACGGACTCCCTGTGTGGGTATTCTGAGCGAGA
TCTTCTGAAAAAGGCCGACT**TAAG**GCTGGGGCTCTGAGGGTACCCCTGTGGCCAGCCCTGAA
GCCCACATTCTGGGGGTGTCGTCAGTGCCTCCGGAGGGCCAGATAGGCCCCGCCAA
AGGGTTCTGCCTGGCGTGGGCTTGGGCCGCTGGGTCCGCCGCTGGCCGGAGGCCCTA
GGAGCTGGTGTGCCCGCCGGCCGGCGAGGAGGAGGCAGGGCCACACTGTGCC
TGAGGCCGGAACCGTTCGCACCCGGCTGCCAGTCAGGCCGTTAGAAGAGCTTTAC
TTGGCGCCCGCCGTCTGGCGGAACACTGGAATGCATATACTACTTATGTGCTGTGTT
TTTATTCTGGATACATTGATTTTACGTAAGTCCACATATACTTCTATAAGAGCGTG
ACTTGTAATAAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 18

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307
><subunit 1 of 1, 548 aa, 1 stop
><MW: 63198, pI: 8.10, NX(S/T): 4
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ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGQGRTGVSVVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDESVIVVLLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRRESFGDPKERVRWRKTQNLD
YCFLMMYAQSkgIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGTH
SSLAGKIQKLKDGFQKALRKEHVNPPEAVSTSLKTYQHFTLEKAYLREDFFWAFTPAAAGD
FIRFRFFQPLRLERFFFSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAGPLEALRLSIQTDSPVWVILSEIFLKKAD
```

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515